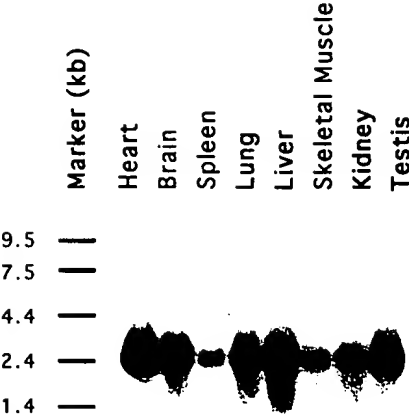


FIG. 2A



FIG. 2B



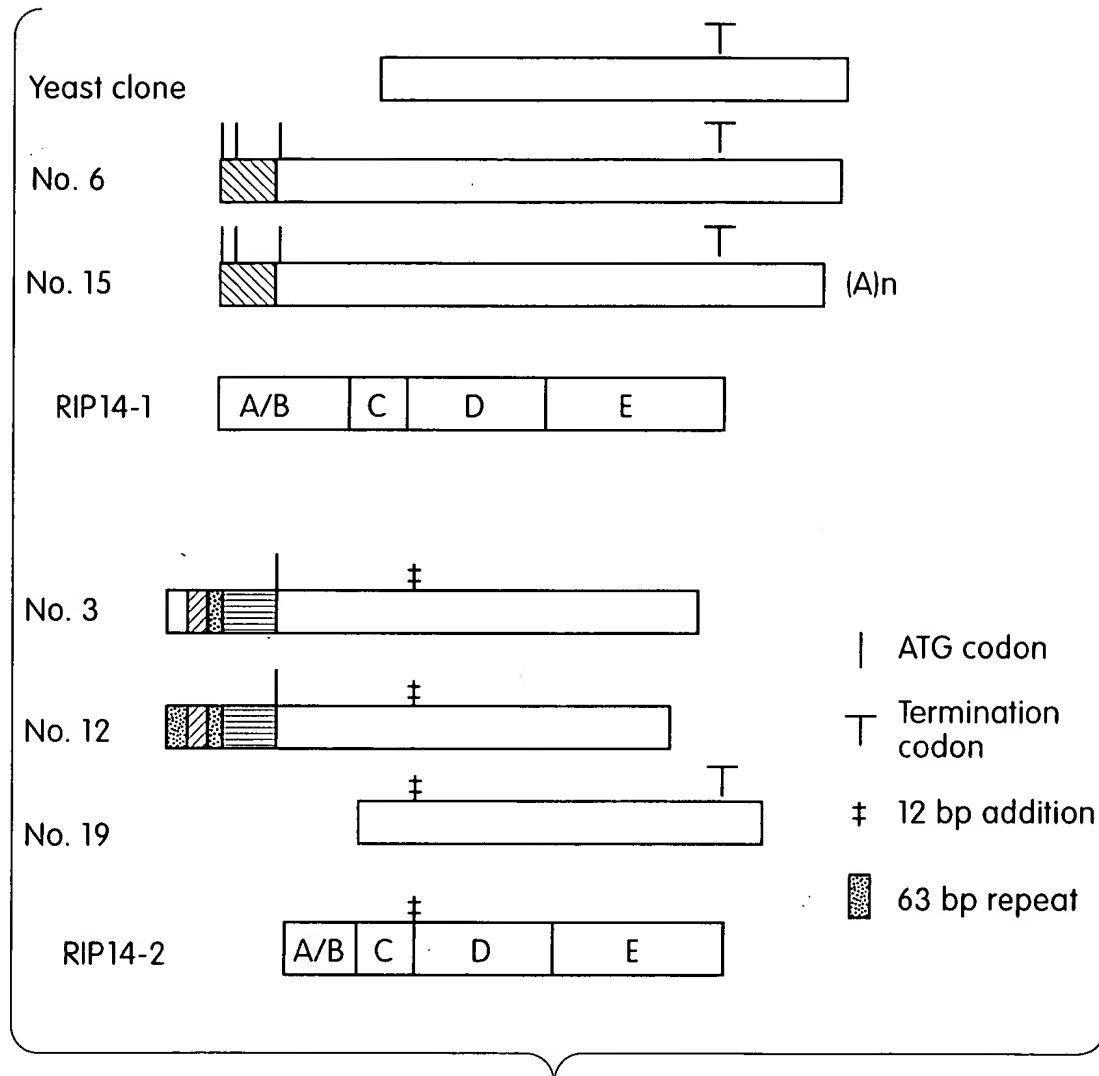


FIG. 3

	RIP14 Clone No		
Specific to RIP14-2 clone 3	3	12	6
TGGTCACCCAGGCTTCTGCTTCAGTCTCTCCTCCTTCTCCTCCTCAGCCCACTGTCTCCT	60	-	-
CATCTCACCCC	71	-	-
Specific to RIP14-2 clone 12			
<u>AAAATTACTGGGCACTAGAAAGGAAGACTGGGCTCCGAATCCTCTTAGAGCCTTGGACAT</u>	-	60	-
<u>CTCACCCG</u>	-	68	-
Common to RIP14-2			
AGAGAAGAACCGAGTTCTGAGAGTCTACAGCAAAATTACTGGGCACTAGAAAGGAAGACT	131	128	-
<u>GGGCTCCGAATCCTCTTAGAGCCTTGGACATCTCTGGCCCAAAGCAATCCAAGGATCTTA</u>	191	188	-
<u>TTTGAGGACCACCATCCCAGAAGTACTTTCTCAAGTTGAAAAGTTGGAGTGGTAGCCAA</u>	251	248	-
GATGAATCTGATTGGGCACTCCATTTACAGGCTACGGACGAGTTTCTCTTTCTGAAAGC	311	308	-
TTATTT	317	314	-
Specific to RIP14-1			
GGAAGCTAAGG ATGGT CATG CAGTTTCAGGGCTTAGAAAATCCAATTCAGATTAGTCTTC	-	-	60
M V M Q F Q G L E N P I Q I S L	-	-	16
ACCACAGCCACCGGCTGTCAGGATTTGTGCCGGACGGG ATG AGTGTGAAGCCAGCTAAA	-	-	119
H H S H R L S G F V P D G M S V K P A K	-	-	36
Common to both isoforms			
GGT ATG CTAACAGAACACGCGGCAGGCCCTCTGGGGCAGAATCTGGATTGGAATCGTACT	378	375	180
G M L T E H A A G P L G Q N L D L E S Y	19	19	56
CCCCATACAACAATGTCCCGTTTCTCAAGTTACGCCACAGATTTCTCCTCGTCTTACT	438	435	240
S P Y N N V P F P Q V Q P Q I S S S S Y	39	39	76
ATTCCAACCTGGGCTTCTACCCCCAACAACCGGAAGACTGGTATTCTCCTGGCATCTATG	498	495	300
Y S N L G F Y P Q Q P E D W Y S P G I Y	59	59	96
AACTCAGGCGAATGCCCCGCTGAGACTGGGTACCAGGGAGAGACTGAGGTATCAGAGATGC	558	555	360
E L R R M P A E T G Y Q G E T E V S E M	79	79	116
CTGTGACAAAGAAGCCGCGAATGGCCGCGGCATCGGCAGGCAGAATAAAAGGGGATGAGC	618	615	420
P V T K K P R M A A A S A G R I K G D E	99	99	136
TGTGTGTTGTCTGTGGAGACAGGGCCTCTGGGTACCACTACAACGCGCTCACCTGTGAGG	678	675	480
L <u>C V V C G D R A S G Y H Y N A L T C E</u>	119	119	156

FIG. 4 (page 1 of 3)

GCTGCAAAGGTTTCTTCCGAAGAAGCATTACCAAGAACGCCGTGTACAAGTGTAAAGAACG	738	735	540
G C K G F F R R S I T K N A V Y K C K N	139	139	176
GGGGCAACTGCGTGATGGACATGTACATGCGCAGGAAGTGCCAGGAGTGCCGGCTAAGGA	798	795	600
G G N C V M D M Y M R R K C Q E C R L R	159	159	196
<div style="display: flex; align-items: center; justify-content: center;"> <div style="border: 1px solid black; padding: 5px; margin-right: 10px;"> GTATGTATACAG M Y T G </div> <div>RIP14-2 specific</div> </div>			
AGTGCAGAGAGATGGGGATGTTGGCTGAAT GTTGTTAAGTAAATCCAGTGTAAATCTA	870	867	660
K C R E M G M L A E C L L T E I Q C K S	183	183	216
AACGGCTAAGGAAAAATGTGAAGCAGCACGCTGATCAGACAGTGAATGAGGACGACAGCG	930	927	720
K R L R K N V K Q H A D Q T V N E D D S	203	203	236
AAGGGCGTGACTTGCGACAAGTGACCTCCACAACCAAGTTTTGCAGGGAGAAAACGGAAC	990	987	780
E G R D L R Q V T S T T K F C R E K T E	223	223	256
TCACGGCAGACCAGCAGACCCCTCCTGGATTATATTATGGATTTCGTACAACAAACAGAGAA	1050	1047	840
L T A D Q Q T L L D Y I M D S Y N K Q R	243	243	276
TGCCCTCAGGAAATCACAAATAAAATCTTAAAGAAGAATTTAGTGCAGAAGAAAATTTTC	1110	1107	900
M P Q E I T N K I L K E E F S A E E N F	263	263	296
TCATATTAACAGAAATGGCAACCAGCCATGTACAGATTCTCGTAGAATTCACAAAAAAGC	1170	1167	960
L I L T E M A T S H V Q I L V E F T K K	283	283	316
TTCCAGGGTTTCAGACACTGGACCACGAAGATCAGATTGCTTTGCTCAAAGGGTCCGCAG	1230	1227	1020
L P G F Q T L D H E D Q I A L L K G S A	303	303	336
TGGAGGCCATGTTTCTTCGTTTCGGCGGAGATTTTCAATAAGAACTTCTTGCCGGACATG	1290	1287	1080
V E A M F L R S A E I F N K K L P A G H	323	323	356
CAGACCTGTTGGAAGAAAGAATTCGAAAGAGTGGTATCTCTGATGAGTATATAACCCCGA	1350	1347	1140
A D L L E E R I R K S G I S D E Y I T P	343	343	376
TGTTTCAGTTTCTATAAAAGTGTGGAGAACTCAAAATGACTCAGGAGGAGTACGCTCTGC	1410	1407	1200
M F S F Y K S V G E L K M T Q E E Y A L	363	363	396
TCACAGCGATCGTCATCCTCTCTCCAGACAGACAATACATCAAGGACAGAGAGGCGGTGG	1470(1453)	1260	
L T A I V I L S P D R Q Y I K D R E A V	383 (378)	416	
AGAAGCTGCAGGAGCCCCTGCTTGATGTGCTACAAAAGCTGTGCAAGATGTACCAGCCTG	1530	-	1320
E K L Q E P L L D V L Q K L C K M Y Q P	403	-	436
AGAACCCACAGCATTTGCGCTGCCTCCTGGGTGCGCTGACGGAAGTCCGGACATTCAACC(1554)	-	-	1380
E N P Q H F A C L L G R L T E L R T F N (411)	-	-	456
ATCACCACGCTGAGATGCTGATGTCTTGAGAGTGAATGATCACAAGTTCACCCCGCTCC	-	-	1440
H H H A E M L M S W R V N D H K F T P L	-	-	476
TCTGTGAGATCTGGGATGTGCAGTGTGACACCAAGTGGGGCTGGCTCCTTGTCTCCTC	-	-	1500
L C E I W D V Q *	-	-	484

FIG. 4 (page 2 of 3)

GGAACAGAAACCTTGTTTCGTTTGTACCTGGTTTCACTCAAGAATCTCAATGAATATTTA	-	-	1560
TGTGGCAATTATACACCTCCCACGGTTGTAAATACAGACTAGATAGAACTGCTTTCCCCA	-	-	1620
CACTGTATTTTACAAGGCTTCAGGAAACCCCACTGGCATGCCCTTTTGGCCTAATTAAAT	-	-	1680
CAATTGTTACTTCAATTCTATCTACTGAGCTAGGGGCATATTATTCTTCATTTCGACAATA	-	-	1740
TTATATATATTTTATAAAGTTGAGCTGTTTCAACTGAGACAATAAA	-	-	1787

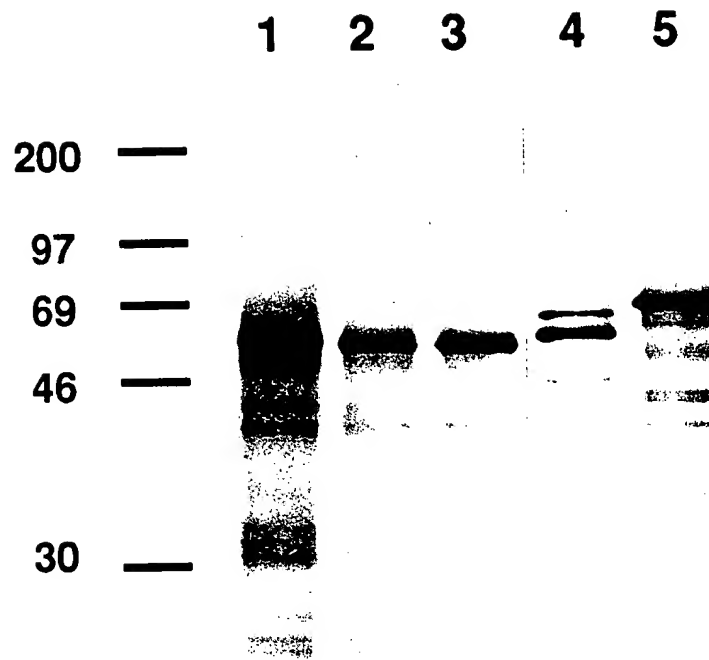
FIG. 4 (page 3 of 3)

GCCAGGGCAACAGAGTCGGAGACCCCCCTGCCACCCCCCTCCCGATCGCCGGTGCAGTCAT -71
 GAGCCCCGCCTCCCCCTGGTGCACGGAGAGGGGCGGGCCTGGAACAAGCAGGCTGCTTC -11
GTGACCCACTATGTCTTCCCCCACAAGTTCTCTGGACACTCCCGTGCCTGGGAATGGTTC 50
 M S S P T S S L D T P V P G N G S 17
 TCCTCAGCCCAGTACCTCCGCCACGTCACCCACTATTAAGGAAGAGGGGCAGGAGACTGA 110
 P Q P S T S A T S P T I K E E G Q E T D 37
 TCCTCCTCCAGGCTCTGAAGGGTCCAGCTCTGCCTACATCGTGGTCATCTTAGAGCCAGA 170
 P P P G S E G S S S A Y I V V I L E P E 57
 GGATGAGCCTGAGCGCAAGCGGAAGAAGGGGCCGCCCCGAAGATGCTGGGCCATGAGCT 230
 D E P E R K R K K G P A P K M L G H E L 77
 GTGCCGCGTGTGCGGAGACAAGGCTTCGGGCTTCCACTACAACGTGCTCAGCTGTGAAGG 290
 C R V C G D K A S G F H Y N V L S C E G 97
CTGCAAAGGCTTCTTCCGGCGCAGTGTGGTCCACGGTGGGGCCGGGCGCTATGCCTGTCTG 350
 C K G F F R R S V V H G G A G R Y A C R 117
 GGGCAGCGGAACCTGCCAGATGGATGCCTTCATGCGGCGCAAGTGCCAGCTCTGCCGGCT 410
 G S G T C Q M D A F M R R K C Q L C R L 137
GCGCAAGTGCAAGGAGGCTGGCATGCGGGAGCAGTGCGTGCTCTCTGAGGAGCAGATTCTG 470
 R K C K E A G M R E Q C V L S E E Q I R 157
 GAAGAAAAGGATTTCAGAAGCAGCAACAGCAGCAGCCACCACCCCATCTGAGCCAGCAGC 530
 K K R I Q K Q Q Q Q Q P P P P S E P A A 177
 CAGCAGCTCAGGCCGGCCAGCGGCCTCCCCTGGCACTTCGGAAGCAAGCAGCCAGGGCTC 590
 S S S G R P A A S P G T S E A S S Q G S 197
 CGGGGAAGGAGAGGGCATCCAGCTGACCGCGGCTCAGGAGCTGATGATCCAGCAGTTAGT 650
 G E G E G I Q L T A A Q E L M I Q Q L V 217
 TGCCGCGCAGCTGCAGTGCAACAAACGATCTTTCTCCGACCAGCCCAAAGTCACGCCCTG 710
 A A Q L Q C N K R S F S D Q P K V T P W 237
 GCCCCTGGGTGCAGACCCTCAGTCCCGAGATGCCCGTCAGCAACGCTTTGCCCACTTCAC 770
 P L G A D P Q S R D A R Q Q R F A H F T 257
 CGAGCTAGCCATCATCTCGGTCCAGGAGATTGTGGACTTTGCCAAGCAGGTGCCAGGGTT 830
 E L A I I S V Q E I V D F A K Q V P G F 277
 CTTGCAGTTGGGCCGGGAGGACCAGATCGCCCTCCTGAAGGCGTCCACCATTGAGATCAT 890
 L Q L G R E D Q I A L L K A S T I E I M 297
 GTTGCTAGAAACAGCCAGACGCTACAACCACGAGACAGAATGCATCACGTTCTCTGAAGGA 950
 L L E T A R R Y N H E T E C I T F L K D 317

FIG. 5 (page 1 of 2)

CTTCACCTACAGCAAGGACGACTTCCACCGTGCAGGCTTGCAGGTGGAATTCATCAATCC	1010
F T Y S K D D F H R A G L Q V E F I N P	337
CATCTTCGAGTTCTCGCGGGCCATGCGGGCGGCTGGGCCTGGACGATGCAGAGTATGCCTT	1070
I F E F S R A M R R L G L D D A E Y A L	357
GCTTATCGCCATCAACATCTTCTCAGCCGATCGGCCTAATGTGCAGGAGCCCAGCCGTGT	1130
L I A I N I F S A D R P N V Q E P S R V	377
GGAGGCCCTGCAGCAGCCCTACGTGGAGGCGCTCCTCTCCTACACGAGGATCAAGCGCCC	1190
E A L Q Q P Y V E A L L S Y T R I K R P	397
ACAGGACCAGTCCGCTTCCCACGCATGCTCATGAAGCTGGTGAGCCTGCGCACCCCTCAG	1250
Q D Q L R F P R M L M K L V S L R T L S	417
CTCCGTGCACTCGGAGCAGGTCTTTGCATTGCGACTCCAGGACAAGAAGCTGCCGCCCTT	1310
S V H S E Q V F A L R L Q D K K L P P L	437
GCTGTCCGAGATCTGGGATGTGCACGAGTAGGGGCAGCCACAAGTGCCCCAGCCTTGGTG	1370
L S E I W D V H E *	446
GTGTCTTCTTGAAGATGGACTCTTCACCTCTCCTCCTGGGGTGGGAGGACATTGTCACGG	1430
CCCAGTCCCTCGGGCTCAGCCTCAAACCTCAGCGGCAGTTGGCACTAAGAAGGCCCCACCC	1490
CACCCATTGAGTCTTCCAAGAGTGGTGAGGGTCACAGGTCCTAGCCTCTGACCGTTCCCA	1550
GCTGCCCTCCCACCCACGCTTACACCTCAGCCTACCACACCATGCACCTTGAGTGGAGAG	1610
AGGTTAGGGCAGGTGGCCCCCAGTTGGGAGACCACAGGCCCTCTCTTCTGCCCCTTT	1670
TATTTAATAAAAAAACAATAAAGTTTGAGTACAAGCCAAAAAAAAAAAAAAAAAAAAA	1730

FIG. 5 (page 2 of 2)

**FIG. 6**

RIP14		DNA		LIGAND/DIMER
EcR		82		37
RIP15		67		42
TR		61		26
RAR		59		31

FIG. 7A

RIP15		DNA		LIGAND/DIMER
EcR		64		42
RAR		56		38
RXR		51		27
TR		50		32

FIG. 7B

			RIP14-1				cell
							lysate
RXR	-	-	+	+	+	-	+
Competitor	-	-	-	sp	ns	-	-

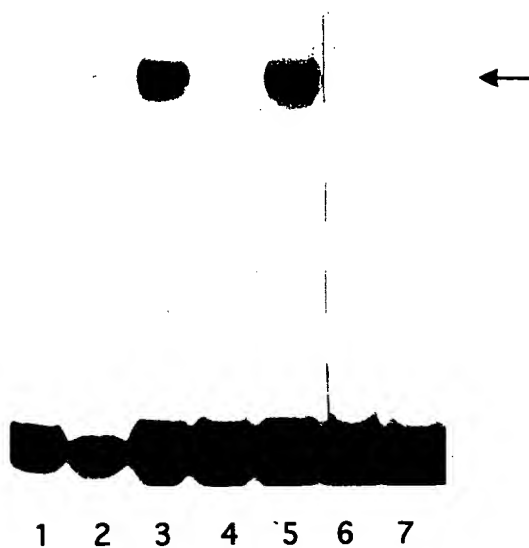


FIG. 8A

			RIP15				cell
							lysate
RXR	-	-	+	+	+	-	+
Competitor	-	-	-	sp	ns	-	-



RIP14-1	-	+	+	+	+	-	-
RIP14-2	-	-	-	-	-	-	+
RIP14C	-	-	-	-	-	+	-
RXR	-	-	+	+	+	+	+
Competitor	-	-	-	sp	ns	-	-



FIG. 8B

```

12  TCTCCAAGTTGTGGCTTTTCAGAGGAAGGATCTGGAAACAAGCAGTTGTGTTCAGTATAAAG 71
    -----+-----+-----+-----+-----+-----+-----+
AGAGGTTCAACACCGAAAGTCTCCTTCCTAGACCTTTGTTTCGTCAACACAGTCATATTC

c   S P S C G F Q R K D L E T S S C V S I K -

    AAGAAGCGTAGACTTGAGGACTTACTCATAGTGATATCCGATAGCGATGGAGAGGAAACA
72  -----+-----+-----+-----+-----+-----+-----+ 131
    TTCTTCGCATCTGAACTCCTGAATGAGTATCACTATAGGCTATCGCTACCTCTCCTTTGT

c   K K R R L E D L L I V I S D S D G E E T -

    AAAGAGGAGAATGGATTGCAGAAAACGAAGACAAAACAGTCGAACAGATCAAAGTGTTTTG
132 -----+-----+-----+-----+-----+-----+-----+ 191
    TTTCTCCTCTTACCTAACGTCTTTTGCTTCTGTTTTGTCAGCTTGTCTAGTTTCACAAAC

c   K E E N G L Q K T K T K Q S N R S K C L -

    GCTAAAAGAAAAGTTGCACACATGTCAGAAGAAGAACAATTTGCTTTGGCTCTCAAGATG
192 -----+-----+-----+-----+-----+-----+-----+ 251
    CGATTTTCTTTTCAACGTGTGTACAGTCTTCTTCTTGTTAAACGAAACCGAGAGTTCTAC

c   A K R K V A H M S E E E Q F A L A L K M -

    AGTGAGCAGGAAGCTAGGGAGGTGAATAACCAGGAGGAGAAAGAAGAGGAGCTCTTGCGG
252 -----+-----+-----+-----+-----+-----+-----+ 311
    TCACTCGTCCTTCGATCCCTCCACTTATTGGTCCTCCTCTTTCTTCTCCTCGAGAACGCC

c   S E Q E A R E V N N Q E E K E E E L L R -

    AAAGCCATTGCTGAAAGCCTGAATAGTTGCTGGTCTTCTGCTGCTTCTGCTACCAGATCT
312 -----+-----+-----+-----+-----+-----+-----+ 371
    TTTCGGTAACGACTTTCGGACTTATCAACGACCAGAAGACGACGAAGACGATGGTCTAGA

c   K A I A E S L N S C W S S A A S A T R S -

    CGACCTCTGGCTGCTGAACTATCTTCACATTCCCATCAAGAGAACACCAAAGACTCTGGG
372 -----+-----+-----+-----+-----+-----+-----+ 431
    GCTGGAGACCGACGACTTGATAGAAGTGTAAGGGTAGTTCTTCTGTGGTTTCTGAGACCC

c   R P L A A E L S S H S H Q E N T K D S G -

    ACCACTGAAGGCGTATGGCAGCTGGTACCTCCATCACTGTGTAAAGGCTCACATGTCAGT
432 -----+-----+-----+-----+-----+-----+-----+ 491
    TGGTGACTTCCGCATACCGTCGACCATGGAGGTAGTGACACATTTCCGAGTGTACAGTCA

c   T T E G V W Q L V P P S L C K G S H V S -

    CAGGGAAACGAGGCTGAGCAAAGAAAGGAGCCCTGGGAcCACAATGAAAACACTGAAGAG
492 -----+-----+-----+-----+-----+-----+-----+ 551
    GTCCCTTTGCTCCGACTCGTTTCTTTCTCGGGACCCTgGTGTTACTTTTGTGACTTCTC

c   Q G N E A E Q R K E P W D H N E N T E E -

    GAGCCGGTCTCTGGCAGCTCAGGAAGCTGGGACCAGTCAAGCCAGCCAGTGTGAGAAT
552 -----+-----+-----+-----+-----+-----+-----+ 611
    CTCGGCCAGAGACCGTCGAGTCCTTCGACCCTGGTCAGTTCCGGTCGGTCACAAACTCTTA

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FIG. 10 (page 1 of 4)

FIG. 10 (page 2 of 4)

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1212 GAAGAAGGTCTGAAGAGTTCGGAAGGAGACAACCTCTGTGCCCACCACGCAAAGCATTGCA 1271
-----+-----+-----+-----+-----+-----+-----+
CTTCTTCCAGACTTCTCAAGCCTTCCTCTGTTGAGACACGGGTGGTGCCTTCGTAACGT

c   E E G L K S S E G D N S V P T T Q S I A -

1272 GCTTTGACCAGTAAGAGAAGTTTAGTTCTTATGCCGGAAGTTCTGCAGAAGAAATCACT 1331
-----+-----+-----+-----+-----+-----+
CGAAACTGGTCATTCTCTTCAAATCAAGAATACGGCCTTCAAGACGTCTTCTTTAGTGA

c   A L T S K R S L V L M P E S S A E E I T -

1332 GTTTGCCCTGAGACACAGTTAAGTTTCCTTGAACCCCTTGACCTCAATAGAGAAGACTCT 1391
-----+-----+-----+-----+-----+-----+
CAAACGGGACTCTGTGTCAATTCAAAGGAACCTGGGGAACTGGAGTTATCTCTTCTGAGA

c   V C P E T Q L S F L E P L D L N R E D S -

1392 CCAGATAGCAGAGAGCTCCCCATTGAAGTAAGGATGGCAGTGGGCGATAAGCAGGTTGCT 1451
-----+-----+-----+-----+-----+-----+
GGTCTATCGTCTCTCGAGGGGTAACTTCATTCCCTACCGTCACCCGCTATTCGTCCAACGA

c   P D S R E L P I E V R M A V G D K Q V A -

1452 AATAGGGAAGATTGTATGAAGGAAAACCTCCTCCTGCAGTCTCATCTAGTACCCGGGTA 1511
-----+-----+-----+-----+-----+-----+
TTATCCCTTCTAACATACTTCCTTTTGGGAGGAGGACGTCAGAGTAGATCATGGGCCCAT

c   N R E D C M K E N P P P A V S S S T R V -

1512 TCCTGCCCCTGTGTAACCAAGACTTTCCTCCCAAAAGATTGAACAGCATGCCATGTAC 1571
-----+-----+-----+-----+-----+-----+
AGGACGGGTGACACATTGGTTCTGAAAGGAGGGTGTTCCTAACTTGTCGTACGGTACATG

c   S C P L C N Q D F P P T K I E Q H A M Y -

1572 TGCAATGGTCTGATGGAGCAGGAAACAGTGTTGACTCGGAGACGAAGAGAGGCCAAGAAC 1631
-----+-----+-----+-----+-----+-----+
ACGTTACCAGACTACCTCGTCCTTTGTCACAACTGAGCCTCTGCTTCTCTCCGGTTCTTG

c   C N G L M E Q E T V L T R R R R E A K N -

1632 AAGAGTGACGGTCGGACAGCTGCACAGCCGGCTCTGGATGCCAACAGGAAGGAGAAGTGT 1691
-----+-----+-----+-----+-----+-----+
TTCTCACTGCCAGCCTGTCGACGTGTCGGCCGAGACCTACGGTTGTCTTCTCTTCACA

c   K S D G R T A A Q P A L D A N R K E K C -

1692 TATCTATGTAAGTCCCTGGTTCCACTTGGGGAGTATCAGTGCCATGTGGAGGCCTGTCTC 1751
-----+-----+-----+-----+-----+-----+
ATAGATACATTCAGGGACCAAGGTGAACCCCTCATAGTCACGGTACACCTCCGGACAGAG

c   Y L C K S L V P L G E Y Q C H V E A C L -

1752 CAGCTTGCAAAGGTTGACAGAGAAGATGGGATTGAAGGGACAAGGAGACCAAGGGTGTGT 1811
-----+-----+-----+-----+-----+-----+
GTCGAACGTTTCCAACGTGTCTTCTACCCTAACTTCCCTGTTTCTCTGGTTCCACACA

c   Q L A K V D R E D G I E G T R R P R V C -

GCACCTGTGGAGGGGAAACAACAGCAGCGGCTGAAGAAGTCAAAGGACAAAGGCCATAGT

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FIG. 10 (page 3 of 4)

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1812 -----+-----+-----+-----+-----+-----+-----+ 1871
      CGTGGACACCTCCCCTTTGTTGTCGTCGCCGACTTCTTCAGTTTCCCTGTTTCCGGTATCA
c      A P V E G K Q Q Q R L K K S K D K G H S -
      CAAGGCCGACTCCTCAGTCTCTTGGAGCAGTCTGAGCATAGGACCACAGGTGTAGAGAAA
1872 -----+-----+-----+-----+-----+-----+-----+ 1931
      GTTCCGGCTGAGGAGTCAGAGAACCTCGTCAGACTCGTATCCTGGTGTCCACATCTCTTT
c      Q G R L L S L L E Q S E H R T T G V E K -
      AAACCCAAGTATTTCGGAAGTAAGAACCCTTCAGGATGCCCTCACCAGAGGTGGAAGAGGCT
1932 -----+-----+-----+-----+-----+-----+-----+ 1991
      TTTGGGTTTCATAAGCCTTCATTCTTGAAGTCCTACGGGAGTGGTCTCCACCTTCTCCGA
c      K P K Y S E V R T F R M P S P E V E E A -
      AGCTGCAGCAGAGAGATGCAGAGTACCCTCTCACAGCTCAACTTAAATGAGTCTCCCATC
1992 -----+-----+-----+-----+-----+-----+-----+ 2051
      TCGACGTCTCTCTCTACGTCTCATGGGAGAGTGTTCGAGTTGAATTTACTCAGAGGGTAG
c      S C S R E M Q S T L S Q L N L N E S P I -
      AAGTCTTTTGTTCCTGTTTCAGAAAGCTACAAATTGCTTAGTGGACTTTAAAGAACAGTTT
2052 -----+-----+-----+-----+-----+-----+-----+ 2111
      TTCAGAAAACAAGGACAAAGTCTTCGATGTTTAAACGAATCACCTGAAATTTCTTGTCAAA
c      K S F V P V S E A T N C L V D F K E Q F -
      GCTTTCCGGTCACGAACATAATCAGGCAGGGAAGGAGGAGAAAAATCTTGAATTTCTTGA
2112 -----+-----+-----+-----+-----+-----+-----+ 2171
      CGAAAGGCCAGTGCCTTGATTTAGTCCGTCCCTTTCTCCTCTTTTAGAACTTAAAGAACT
c      A F R S R T K S G R E R R R K S *
      GACTGGAAGGTTGACCAGAACACACATCGTTGGGTTGATCGTGTTCATTAAGTATAGTGG
2172 -----+-----+-----+-----+-----+-----+-----+ 2231
      CTGACCTTCCAACGGTCTTGTGTGTAGCAACCAACTAGCACAAAGTAATTCATATCACC
      TCTCTAGTTTGTGGTGAGAGTTCTGACCCTGTTGTTATCACCACCAGCACCCATTAGTA
2232 -----+-----+-----+-----+-----+-----+-----+ 2291
      AGAGATCAAACACCACCTCAAGACTGGGACAACAATAGTGGTGGTCGTGGGTAAGTCAT
      TCCTGGCTTTTATATTTTATAAGATCAGTTCAGACAACTGTGAATATTATTCTGTTTGAAT
2292 -----+-----+-----+-----+-----+-----+-----+ 2351
      AGGACCGAAATATAAAATATTCTAGTCAAGTCTGTTGACACTTATAATAAGACAACTTA
      TTGCTTATAGTTAAAAATTTAAATATATTTATCTTTGTATGAAAAAAAAA
2352 -----+-----+-----+-----+-----+-----+-----+
      AACGAATATCAATTTTAAATTTATATAAATAGAAACATACTTTTTTTTTT

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FIG. 10 (page 4 of 4)

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          GGATGCCCTGGCTGCTCTTGTGGATGCTGCAGCTTCTGCACCCAGATGGATGTTTCCAA
901  -----+-----+-----+-----+-----+-----+ 960
          CCTACGGGACCGACGAGAACACCTACGACGTCTGAAGACGTGGGGTCTACCTACAAAGGTT

b      D A L A A L V D A A A S A P Q M D V S K -

          AACAAAAGAGAGTAAGCATGAAGCTGCCAGGTTAGAAGAAAATTTGAGAAGCAGGTCAGC
961  -----+-----+-----+-----+-----+-----+ 1020
          TTGTTTTCTCTCATTTCGTACTTCGACGGTCCAATCTTCTTTAAACTCTTCGTCCAGTCG

b      T K E S K H E A A R L E E N L R S R S A -

          AGCAGTTAGTGAACAGCAGCAGCTAGAGCAGAAAAACCTGGAGGTGGAGAAGAGATCTGT
1021 -----+-----+-----+-----+-----+-----+ 1080
          TCGTCAATCACTTGTCTGTCGTCGATCTCGTCTTTTGGACCTCCACCTCTTCTCTAGACA

b      A V S E Q Q Q L E Q K N L E V E K R S V -

          TCAGTGTGTGCACTTCTTCAGCCCTTCCAAGTGGCAAGGCCAGCCTCATGCCTCAGT
1081 -----+-----+-----+-----+-----+-----+ 1140
          AGTCACACACACGTGAAGAAGTCGGAAGGTTCAACCGTTCCGGGTCGGAGTACGGAGTCA

b      Q C V C T S S A L P S G K A Q P H A S V -

          AGTGTATTCTGAGGCTGGGAAAGATAAAGGGCCTCCTCCAAAATCCAGATATGAGGAAGA
1141 -----+-----+-----+-----+-----+-----+ 1200
          TCACATAAGACTCCGACCCTTTCTATTTCCCGAGGAGGTTTATAGGTCTATACTCCTTCT

b      V Y S E A G K D K G P P P K S R Y E E E -

          GCTAAGGACCCGAGGGAAGACTACCATTACTGCAGCTAACTTCATAGACGTGACCATCAC
1201 -----+-----+-----+-----+-----+-----+ 1260
          CGATTCTGGGCTCCCTTCTGATGGTAATGACGTCGATTGAAGTATCTGCACTGGTAGTG

b      L R T R G K T T I T A A N F I D V T I T -

          CCGGCAAATTGCCTCGGACAAGGATGCGAGGGAACGTGGCTCTCAAAGTTCAGACTCTTC
1261 -----+-----+-----+-----+-----+-----+ 1320
          GGCCGTTTAAACGGAGCCTGTTCTACGCTCCCTTGACCCGAGAGTTTCAAGTCTGAGAAG

b      R Q I A S D K D A R E R G S Q S S D S S -

          TAGTAGCTTGTCTTCTCACAGGTATGAAACGGCTAGTGATGCCATTGAGGTGATAAGTCC
1321 -----+-----+-----+-----+-----+-----+ 1380
          ATCATCGAACAGAAGAGTGTCCATACTTTGCCGATCACTACGGTAACTCCACTATTTCAGG

b      S S L S S H R Y E T A S D A I E V I S P -

          CGCCAGCTCACCTGCACCACCCAGGAAAAGCCACAGGCCTATCAGCCAGACATGGTTAA
1381 -----+-----+-----+-----+-----+-----+ 1440
          GCGGTCTGAGTGGACGTGGTGGGGTCTTTTCGGTGTCCGATAGTCCGGTCTGTACCAATT

b      A S S P A P P Q E K P Q A Y Q P D M V K -

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FIG. 11 (page 1 of 4)

1441 GGCAAATCAAGCAGAAAATGAGTCCACTCGACAGTATGAAGGTCCACTGCATCATTATCG
 -----+-----+-----+-----+-----+-----+ 1500
 CCGTTTAGTTCGTCTTTTACTCAGGTGAGCTGTCATACTTCCAGGTGACGTAGTAATAGC
 b A N Q A E N E S T R Q Y E G P L H H Y R -
 1501 GTCCCAGCAGGAATCACCATCTCCACAGCAACAGCCACCCTGCCCCATCTTCCCAGTC
 -----+-----+-----+-----+-----+ 1560
 CAGGGTCGTCCTTAGTGGTAGAGGTGTCGTTGTCGGTGGTGACGGGGGTAGAAGGGTCAG
 b S Q Q E S P S P Q Q Q P P L P P S S Q S -
 1561 AGAGGGAATGGGACAGGTGCCCAGGACCCATCGACTGATCACACTTGCTGACCACATCTG
 -----+-----+-----+-----+-----+ 1620
 TCTCCCTTACCCTGTCCACGGGTCCTGGGTAGCTGACTAGTGTGAACGACTGGTGTAGAC
 b E G M G Q V P R T H R L I T L A D H I C -
 1621 TCAAATTATCACACAAGATTTTGTAGAAATCAAGTTCCCTCGCAGCCTTCTACTTCTAC
 -----+-----+-----+-----+-----+ 1680
 AGTTTAATAGTGTGTTCTAAAACGATCTTTAGTTCAAGGGAGCGTCGGAAGATGAAGATG
 b Q I I T Q D F A R N Q V P S Q P S T S T -
 1681 ATTCCAAACTTCACCATCTGCTTTGTTCATCCACACCTGTAAGAACTAAAACCTCAAGCCG
 -----+-----+-----+-----+-----+ 1740
 TAAGGTTTGAAGTGGTAGACGAAACAGTAGGTGTGGACATTCTTGATTTTGAGTTCCGGC
 b F Q T S P S A L S S T P V R T K T S S R -
 1741 CTACAGCCCAGAATCACAGTCTCAGACTGTCTTGCATCCCAGACCAGGTCTTAGAGTCTC
 -----+-----+-----+-----+-----+ 1800
 GATGTCGGGTCTTAGTGTGAGTCTGACAGAACGTAGGGTCTGGTCCAGGATCTCAGAG
 b Y S P E S Q S Q T V L H P R P G P R V S -
 1801 TCCAGAAAATCTTGTGGATAAATCCCGGGGAAGCAGGCCTGGAAAATCTCCAGAGAGGAG
 -----+-----+-----+-----+-----+ 1860
 AGGTCTTTTAGAACACCTATTTAGGGCCCTTCGTCGCGACCTTTTAGAGGTCTCTCCTC
 b P E N L V D K S R G S R P G K S P E R S -
 1861 TCATATCCCATCAGAGCCCTATGAGCCCATCTCCCCACCCCAAGGCCCTGCTGTGCATGA
 -----+-----+-----+-----+-----+ 1920
 AGTATAGGGTAGTCTCGGGATACTCGGGTAGAGGGTGGGGTCCGGGACGACACGTA
 b H I P S E P Y E P I S P P Q G P A V H E -
 1921 GAAGCAGGACAGCATGTTGCTCTTGTACAGAGGGGAGTGGACCTGCTGAGCAAAGGAG
 -----+-----+-----+-----+-----+ 1980
 CTTGTCCTGTCGTACAACGAGAACAGTGTCTCCCTCACCTGGGACGACTCGTTTCCTC
 b K Q D S M L L L S Q R G V D P A E Q R S -
 1981 TGATTCTCGATCACCAGGAAGTATAAGCTACTTGCCTTCATTCTTCACCAAGCTTGAAAG
 -----+-----+-----+-----+-----+ 2040
 ACTAAGAGCTAGTGGTCTTCATATTCGATGAACGGAAGTAAGAAGTGGTTCGAACTTTC
 b D S R S P G S I S Y L P S F F T K L E S -
 CACATCACCCATGGTTAAATCAAAGAAACAGGAAATTTTTCGTAAGTTGAACTCTTCTGG

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2041 -----+-----+-----+-----+-----+-----+ 2100
      GTGTAGTGGGTACCAATTTAGTTTCTTTGTCCTTTAAAAAGCATTCAACTTGAGAAGACC
b      T S P M V K S K K Q E I F R K L N S S G -

      TGGAGGTGACTCTGATATGGCAGCTGCTCAGCCAGGAACAGAGATCTTCAATCTGCCAGC
2101 -----+-----+-----+-----+-----+ 2160
      ACCTCCACTGAGACTATACCGTCGACGAGTCGGTCCCTTGTCTCTAGAAGTTAGACGGTCG
b      G G D S D M A A A Q P G T E I F N L P A -

      AGTTACCACATCAGGTGCAGTGAGCTCAAGAAGCCATTCTTTTGCTGATCCCGCCAGTAA
2161 -----+-----+-----+-----+-----+ 2220
      TCAATGGTGTAGTCCACGTCACTCGAGTCTTCGGTAAGAAAACGACTAGGGCGGTCAATT
b      V T T S G A V S S R S H S F A D P A S N -

      CCTTGGTCTAGAAGACATCATCAGAAAGGCTCTCATGGGAAGTTTTGATGATAAAGTTGA
2221 -----+-----+-----+-----+-----+ 2280
      GGAACCAGATCTTCTGTAGTAGTCTTTCGAGAGTACCCTTCAAACTACTATTTCAACT
b      L G L E D I I R K A L M G S F D D K V E -

      AGATCATGGTGTGTGTCATGTCCCATCCTGTGGGCATTATGCCTGGTAGTGCCAGCACCTC
2281 -----+-----+-----+-----+-----+ 2340
      TCTAGTACCACAACAGTACAGGGTAGGACACCCGTAATACGGACCATCACGGTCGTGGAG
b      D H G V V M S H P V G I M P G S A S T S -

      AGTGGTGACGAGCAGCGAGGCACGGAGAGATGAAGGGGAGCCATCACCTCATGCAGGAGT
2341 -----+-----+-----+-----+-----+ 2400
      TCACCCTGCTCGTCGCTCCGTGCCTCTCTACTTCCCCTCGGTAGTGGAGTACGTCCTCA
b      V V T S S E A R R D E G E P S P H A G V -

      ATGCAAACCAAAGCTGATCAACAAATCAAAACAGCAGGAAGTCTAAATCTCCTATTCTCTGG
2401 -----+-----+-----+-----+-----+ 2460
      TACGTTTGGTTTCGACTAGTTGTTAGTTTGTGTCCTTCAGATTTAGAGGATAAGGACC
b      C K P K L I N K S N S R K S K S P I P G -

      GCAAAGCTATTTAGGAACTGAAAGGCCTTCTTCTGTCTCTCTGTGCATTTCAGAAGGTGA
2461 -----+-----+-----+-----+-----+ 2520
      CGTTTCGATAAATCCTTGACTTTCGGAAGAAGACAGAGGAGACACGTAAGTCTTCCACT
b      Q S Y L G T E R P S S V S S V H S E G D -

      TTACCACAGGCAGACACCAGGATGGGCATGGGAAGATCGGCCCTCTTCAACAGGTTCTAC
2521 -----+-----+-----+-----+-----+ 2580
      AATGGTGTCCGTCTGTGGTCCTACCCGTACCCTTCTAGCCGGGAGAAGTTGTCCAAGATG
b      Y H R Q T P G W A W E D R P S S T G S T -

      TCAGTTCCCTTACAACCCTCTGACCATACGGATGCTCAGCAGTACACCACCTACACAGAT
2581 -----+-----+-----+-----+-----+ 2640
      AGTCAAGGGAATGTTGGGAGACTGGTATGCCTACGAGTCGTCATGTGGTGGATGTGTCTA
b      Q F P Y N P L T I R M L S S T P P T Q I -

      CGCATGCGCCCCATCTGCCATCACCCAAGCAGCTCCACATCAACAGAACCGCATCTGGGA
2641 -----+-----+-----+-----+-----+ 2700
      GCGTACGCGGGGTAGACGGTAGTGGGTTTCGTGAGGTGTAGTTGTCTTGGCGTAGACCTT

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FIG. 11 (page 3 of 4)

b A C A P S A I T Q A A P H Q Q N R I W E -
2701 GAGGGAGCCTGCCCCGCTCCTCTCAGCGCAGTATGAGACACTGTCTGATAGTGACGACTG
-----+-----+-----+-----+-----+-----+ 2760
CTCCCTCGGACGGGGCGAGGAGAGTCGCGTCATACTCTGTGACAGACTATCACTGCTGAC
b R E P A P L L S A Q Y E T L S D S D D * -
2761 AGCTGTGCGTGGGAGAGCGCTCTGGCTTTGGTTTTTATTGAAGATTAAAAAAAAAAAAA
-----+-----+-----+-----+-----+-----+ 2820
TCGACACGCACCCTCTCGCGAGACCGAAACCAAAAATAACTTCTAAATTaTTTTTTTTTT
AA
2821 -- 2822
TT

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